

## SEQUENCE LISTING

<110> Bennett, Michele  
Brodbeck, Robbin  
Krause, James

<120> Chimeric Neuropeptide Y Receptors

<130> N2000.001

<140> Not Yet Assigned

<141> 2000-01-28

<160> 31

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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<223> Description of Artificial Sequence:Y5/Y1 CHIMERA

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 Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg  
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 ttactatctt ctttattgct agttcagtat attctgccct tagtttgtct tactgtaagt 720  
 catacaagtg tctgcagaag tataagctgt ggattgtcca acaaagaaaa cagacttgaa 780  
 gaaaatgaga tgatcaactt aactcttcat ccattccaaa agagtgggct tcaggtgaaa 840  
 ctctctggca gccataaatg gagttattca ttcattcaaa aacacagaag aagatatagc 900  
 aagaagacag catgtgtgtt acctgtcca gaaagacctt ctcaagagaa ccaactccaga 960  
 atacttccag aaaacttttg ctctgtaaga agtcagctct cttcatccag taagttcata 1020  
 ccaggggtcc ccacttgctt tgagataaaa cctgaagaaa attcagatgt tcatgaattg 1080  
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 accatactga tattagtatt tgctgttagt tggatgccac tacacctttt ccatgtggta 1200  
 actgatttta atgacaatct tatttcaaat aggcatttca agttgggtga ttgcatattg 1260  
 catttggttg gcatgatgtc ctgttctctt aatccaattc tatatgggtt tcttaataat 1320  
 ggaattcaga gagacttgca gttcttcttc aacttttctg atttcgggtc tcgggatgat 1380  
 gattatgaaa caatagccat gtccacgatg cacacagatg tttccaaaac ttctttgaag 1440  
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<210> 8  
 <211> 1201  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Y5/Y1 CHIMERA

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 tgatttccca gtctgggatg actataaaaag cagtgtagat gacttacagt attttctgat 180  
 tgggctctat acatttgtaa gtcttcttgg ctttatgggg aatctactta ttttaattgg 240

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tctcatgaaa aagcgtaatc agaagactac ggtaaacttc ctcataggca atctggcctt 300
ttctgatatc ttggttggtc tgttttgctc acctttcaca ctgacgtctg tcttgctgga 360
tcagtggatg tttggcaaag tcatgtgcc aattatgcct tttcttcaat gtgtgtcagt 420
tttggtttca actttaattt taatatcaat tgccattgtc aggtatcata tgataaaaca 480
tcccatatct aataatttaa cagcaaacca tggctacttt ctgatagcta ctgtctggac 540
actaggtttt gccatctgtt ctccccttcc agtgtttcac agtcttggtg aacttcaaga 600
aacatttggt tcagcattgc tgagcagcag gtatttatgt gttgagtcac ggccatctga 660
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ttgtcttact gtaagtcata caagtgtctg catacgcta aaaaggagaa acaacatgat 780
ggacaagatg agagacaata agtacaggc cagtagatct cgaagtgttt tctacagact 840
gaccatactg atattagtat ttgctgttag ttggatgcc ctacaccttt tccatgtggt 900
aactgatttt aatgacaatc ttatttcaaa taggcatttc aagttggtgt attgcatttg 960
tcatttggtg ggcatgatgt cctgttgtct taatccaatt ctatatgggt ttcttaataa 1020
tggaattcag agagacttgc agttcttctt caacttttgt gatttccggt ctcgggatga 1080
tgattatgaa acaatagcca tgtccacgat gcacacagat gtttccaaaa cttctttgaa 1140
gcaagcaagc ccagtcgcat ttaaaaaaat caacaacaat gatgataatg aaaaaatctg 1200
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<210> 9
<211> 499
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:Y5/Y1 CHIMERA

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<400> 9
Met Ser Phe Tyr Ser Lys Gln Asp Tyr Asn Met Asp Leu Glu Leu Asp
 1             5             10            15

Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr
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Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp
      35             40             45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu
      50             55             60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg
      65             70             75             80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser
      85             90             95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val
      100            105            110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro
      115            120            125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser
      130            135            140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn
      145            150            155            160

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Ile Ala Met Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys  
465 470 475 480

Gln Ala Ser Pro Val Ala Phe Lys Lys Ile Asn Asn Asn Asp Asp Asn  
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Glu Lys Ile

$\langle 210 \rangle$  10

<211> 394

&lt;212&gt; PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Y5/Y1 CHIMERA

<400> 10

Met Ser Phe Tyr Ser Lys Gln Asp Tyr Asn Met Asp Leu Glu Leu Asp  
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Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr  
20 25 30

Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp  
35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu  
50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg  
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser  
85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val  
 . 100 105 110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro  
115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser  
130 135 140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn  
145 150 155 160

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu  
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu  
180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys

# 2025

195					200					205					
Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile	Ser
210					215					220					
Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	Val	Cys	Leu	Thr	Val	Ser
225					230					235					240
His	Thr	Ser	Val	Cys	Ile	Arg	Leu	Lys	Arg	Arg	Asn	Asn	Met	Met	Asp
				245					250					255	
Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	Ser	Ser	Arg	Ser	Arg	Ser	Val	Phe
			260					265					270		
Tyr	Arg	Leu	Thr	Ile	Leu	Ile	Leu	Val	Phe	Ala	Val	Ser	Trp	Met	Pro
			275				280					285			
Leu	His	Leu	Phe	His	Val	Val	Thr	Asp	Phe	Asn	Asp	Asn	Leu	Ile	Ser
			290				295				300				
Asn	Arg	His	Phe	Lys	Leu	Val	Tyr	Cys	Ile	Cys	His	Leu	Leu	Gly	Met
305					310					315					320
Met	Ser	Cys	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	Gly	Phe	Leu	Asn	Asn	Gly
				325					330					335	
Ile	Gln	Arg	Asp	Leu	Gln	Phe	Phe	Phe	Asn	Phe	Cys	Asp	Phe	Arg	Ser
			340				345						350		
Arg	Asp	Asp	Asp	Tyr	Glu	Thr	Ile	Ala	Met	Ser	Thr	Met	His	Thr	Asp
			355				360					365			
Val	Ser	Lys	Thr	Ser	Leu	Lys	Gln	Ala	Ser	Pro	Val	Ala	Phe	Lys	Lys
			370			375				380					
Ile	Asn	Asn	Asn	Asp	Asp	Asn	Glu	Lys	Ile						
385					390										

<210> 11

<211> 6

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence:HEXAHISTADINE  
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<400> 11

His His His His His His  
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<210> 12

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:FLAG EPITOPE  
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<400> 12

Asp Tyr Lys Asp Asp Asp Asp Lys  
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<210> 13

<211> 455

<212> PRT

<213> Homo sapiens

<400> 13

Met Ser Phe Tyr Ser Lys Gln Asp Tyr Asn Met Asp Leu Glu Leu Asp  
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Glu Tyr Tyr Asn Lys Thr Leu Ala Thr Glu Asn Asn Thr Ala Ala Thr  
20 25 30

Arg Asn Ser Asp Phe Pro Val Trp Asp Asp Tyr Lys Ser Ser Val Asp  
35 40 45

Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr Thr Phe Val Ser Leu Leu  
50 55 60

Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg  
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser  
85 90 95

Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val  
100 105 110

Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro  
115 120 125

Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser  
130 135 140

Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn  
145 150 155 160

Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu  
165 170 175

Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu  
180 185 190

Leu Gln Glu Thr Phe Gly Ser Ala Leu Leu Ser Ser Arg Tyr Leu Cys  
195 200 205

Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser  
210 215 220

Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu Val Cys Leu Thr Val Ser  
 225 230 235 240  
 His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu  
 245 250 255  
 Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser  
 260 265 270  
 Lys Lys Ser Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser  
 275 280 285  
 Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala  
 290 295 300  
 Cys Val Leu Pro Ala Pro Glu Arg Pro Ser Gln Glu Asn His Ser Arg  
 305 310 315 320  
 Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser  
 325 330 335  
 Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu  
 340 345 350  
 Glu Asn Ser Asp Val His Glu Leu Arg Val Lys Arg Ser Val Thr Arg  
 355 360 365  
 Ile Lys Lys Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile  
 370 375 380  
 Leu Val Phe Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val  
 385 390 395 400  
 Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val  
 405 410 415  
 Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro  
 420 425 430  
 Ile Leu Tyr Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Val Ser  
 435 440 445  
 Leu Ile His Cys Leu His Met  
 450 455

<210> 14  
 <211> 21  
 <212> DNA  
 <213> Homo sapiens

<400> 14  
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<210> 15



<400> 19  
cagcttgaat tccattatta agaaaccc

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<210> 20  
<211> 341  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 20  
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Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp  
20 25 30  
Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr  
35 40 45  
Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met  
50 55 60  
Ala Leu Met Arg Lys Arg Asn Gln Lys Thr Met Val Asn Phe Leu Ile  
65 70 75 80  
Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro  
85 90 95  
Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val  
100 105 110  
Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser  
115 120 125  
Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys  
130 135 140  
His Pro Ile Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile  
145 150 155 160  
Ala Thr Val Trp Thr Leu Gly Phe Ala Ile Cys Ser Pro Leu Pro Val  
165 170 175  
Phe His Ser Leu Val Glu Leu Gln Glu Thr Phe Asp Ser Ala Leu Leu  
180 185 190  
Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg  
195 200 205  
Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu  
210 215 220  
Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg

TrpAspTyrGlu

225                      230                      235                      240  
 Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser  
                                  245                      250                      255  
 Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe  
                                  260                      265                      270  
 Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe  
                                  275                      280                      285  
 Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile  
                                  290                      295                      300  
 Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr  
 305                                   310                      315                      320  
 Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Ile Ser Leu Ile Gln  
                                  325                      330                      335  
 Cys Leu His Met Ser  
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<210> 21  
 <211> 383  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 21  
 Met Asp Leu Glu Leu Gln Asp Phe Tyr Asn Lys Thr Leu Ala Thr Glu  
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 Asn Asn Thr Ala Ala Thr Arg Asn Ser Asp Phe Pro Val Trp Asp Asp  
                                  20                                      25                                      30  
 Tyr Lys Ser Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr  
                                  35                                      40                                      45  
 Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met  
                                  50                                      55                                      60  
 Ala Leu Met Arg Lys Arg Asn Gln Lys Thr Met Val Asn Phe Leu Ile  
   65                                      70                                      75                                      80  
 Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro  
                                  85                                      90                                      95  
 Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val  
                                  100                                      105                                      110  
 Met Cys His Ile Met Pro Phe Leu Gln Cys Val Ser Val Leu Val Ser  
                                  115                                      120                                      125

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Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	130	135	140
His	Pro	Ile	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	145	150	155
Ala	Thr	Val	Trp	Thr	Leu	Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	165	170	175
Phe	His	Ser	Leu	Val	Glu	Leu	Gln	Glu	Thr	Phe	Asp	Ser	Ala	Leu	Leu	180	185	190
Ser	Ser	Arg	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	195	200	205
Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	210	215	220
Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys	Ile	Arg	Leu	Lys	Arg	225	230	235
Arg	Asn	Asn	Met	Met	Asp	Lys	Met	Arg	Asp	Asn	Lys	Tyr	Arg	Ser	Ser	245	250	255
Arg	Ser	Arg	Ser	Val	Phe	Tyr	Arg	Leu	Thr	Ile	Leu	Ile	Leu	Val	Phe	260	265	270
Ala	Val	Ser	Trp	Met	Pro	Leu	His	Leu	Phe	His	Val	Val	Thr	Asp	Phe	275	280	285
Asn	Asp	Asn	Leu	Ile	Ser	Asn	Arg	His	Phe	Lys	Leu	Val	Tyr	Cys	Ile	290	295	300
Cys	His	Leu	Leu	Gly	Met	Met	Ser	Cys	Cys	Leu	Asn	Pro	Ile	Leu	Tyr	305	310	315
Gly	Phe	Leu	Asn	Asn	Gly	Ile	Gln	Arg	Asp	Leu	Gln	Phe	Phe	Phe	Asn	325	330	335
Phe	Cys	Asp	Phe	Arg	Ser	Arg	Asp	Asp	Asp	Tyr	Glu	Thr	Ile	Ala	Met	340	345	350
Ser	Thr	Met	His	Thr	Asp	Val	Ser	Lys	Thr	Ser	Leu	Lys	Gln	Ala	Ser	355	360	365
Pro	Val	Ala	Phe	Lys	Lys	Ile	Asn	Asn	Asp	Asp	Asn	Glu	Lys	Ile		370	375	380

<210> 22

<211> 508

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 22

Met	Glu	Val	Lys	Leu	Glu	Glu	His	Phe	Asn	Lys	Thr	Phe	Val	Thr	Glu	
1				5					10					15		
Asn	Asn	Thr	Ala	Ala	Ser	Gln	Asn	Thr	Ala	Ser	Pro	Ala	Trp	Glu	Asp	
			20					25					30			
Tyr	Arg	Gly	Thr	Glu	Asn	Asn	Thr	Ser	Ala	Ala	Arg	Asn	Thr	Ala	Phe	
		35					40					45				
Pro	Val	Trp	Glu	Asp	Tyr	Arg	Gly	Ser	Val	Asp	Asp	Leu	Gln	Tyr	Phe	
	50					55					60					
Leu	Ile	Gly	Leu	Tyr	Thr	Phe	Val	Ser	Leu	Leu	Gly	Phe	Met	Gly	Asn	
65					70					75					80	
Leu	Leu	Ile	Leu	Met	Ala	Val	Met	Lys	Lys	Arg	Asn	Gln	Lys	Thr	Thr	
				85					90					95		
Val	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Phe	Ser	Asp	Ile	Leu	Val	Val	
			100					105					110			
Leu	Phe	Cys	Ser	Pro	Phe	Thr	Leu	Thr	Ser	Val	Leu	Leu	Asp	Gln	Trp	
		115					120					125				
Met	Phe	Gly	Lys	Ala	Met	Cys	His	Ile	Met	Pro	Phe	Leu	Gln	Cys	Val	
	130					135					140					
Ser	Val	Leu	Val	Ser	Thr	Leu	Ile	Leu	Ile	Ser	Ile	Ala	Ile	Val	Arg	
145					150					155					160	
Tyr	His	Met	Ile	Lys	His	Pro	Ile	Ser	Asn	Asn	Leu	Thr	Ala	Asn	His	
				165					170					175		
Gly	Tyr	Phe	Leu	Ile	Ala	Thr	Val	Trp	Thr	Leu	Gly	Phe	Ala	Ile	Cys	
			180					185					190			
Ser	Pro	Phe	Pro	Val	Phe	His	Ser	Leu	Val	Glu	Leu	Lys	Glu	Thr	Phe	
		195					200					205				
Gly	Ser	Ala	Leu	Leu	Ser	Ser	Lys	Tyr	Leu	Cys	Val	Glu	Ser	Trp	Pro	
	210					215					220					
Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile	Ser	Leu	Leu	Leu	Val	Gln	
225					230					235					240	
Tyr	Ile	Leu	Pro	Leu	Val	Cys	Leu	Thr	Val	Ser	His	Thr	Ser	Val	Cys	
				245					250					255		
Arg	Ser	Ile	Ser	Cys	Gly	Leu	Ser	His	Lys	Glu	Asn	Arg	Leu	Glu	Glu	
			260					265					270			
Asn	Glu	Met	Ile	Asn	Leu	Thr	Leu	His	Pro	Ser	Lys	Lys	Ser	Arg	Asp	
		275					280					285				
Gln	Ala	Lys	Pro	Pro	Ser	Thr	Gln	Lys	Trp	Ser	Tyr	Ser	Phe	Ile	Arg	
	290					295					300					

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Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala Cys Val Leu Pro Ala  
 305 310 315 320  
 Pro Ala Gly Pro Ser Gln Glu Lys His Leu Thr Val Pro Glu Asn Pro  
 325 330 335  
 Gly Ser Val Arg Ser Gln Leu Ser Pro Ser Ser Lys Val Ile Pro Gly  
 340 345 350  
 Val Pro Ile Cys Phe Glu Val Lys Pro Glu Glu Ser Ser Asp Ala Gln  
 355 360 365  
 Glu Met Arg Val Lys Arg Ser Leu Thr Arg Ile Lys Lys Arg Ser Arg  
 370 375 380  
 Ser Val Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser  
 385 390 395 400  
 Trp Met Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn  
 405 410 415  
 Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu  
 420 425 430  
 Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu  
 435 440 445  
 Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp  
 450 455 460  
 Phe Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met  
 465 470 475 480  
 His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala  
 485 490 495  
 Phe Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Val  
 500 505

<210> 23  
 <211> 352  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 23  
 Met Asp Val Leu Phe Phe His Gln Asp Ser Ser Met Glu Phe Lys Leu  
 1 5 10 15  
 Glu Glu His Phe Asn Lys Thr Phe Val Thr Glu Asn Asn Thr Ala Ala  
 20 25 30  
 Ala Arg Asn Ala Ala Phe Pro Ala Trp Glu Asp Tyr Arg Gly Ser Val



340

345

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&lt;210&gt; 24

&lt;211&gt; 499

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:Y1/Y5 CHIMERA

&lt;400&gt; 24

Met	Asp	Val	Leu	Phe	Phe	His	Gln	Asp	Ser	Ser	Met	Glu	Phe	Lys	Leu
1				5					10					15	

Glu	Glu	His	Phe	Asn	Lys	Thr	Phe	Val	Thr	Glu	Asn	Asn	Thr	Ala	Ala
			20					25					30		

Ala	Arg	Asn	Ala	Ala	Phe	Pro	Ala	Trp	Glu	Asp	Tyr	Arg	Gly	Ser	Val
		35					40					45			

Asp	Asp	Leu	Gln	Tyr	Phe	Leu	Ile	Gly	Leu	Tyr	Thr	Phe	Val	Ser	Leu
	50					55					60				

Leu	Gly	Phe	Met	Gly	Asn	Leu	Leu	Ile	Leu	Met	Ala	Val	Met	Lys	Lys
65					70					75					80

Arg	Asn	Gln	Lys	Thr	Thr	Val	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Phe
				85					90					95	

Ser	Asp	Ile	Leu	Val	Val	Leu	Phe	Cys	Ser	Pro	Phe	Thr	Leu	Thr	Ser
			100					105					110		

Val	Leu	Leu	Asp	Gln	Trp	Met	Phe	Gly	Lys	Ala	Met	Cys	His	Ile	Met
		115					120					125			

Pro	Phe	Leu	Gln	Cys	Val	Ser	Val	Leu	Val	Ser	Thr	Leu	Ile	Leu	Ile
		130				135					140				

Ser	Ile	Ala	Ile	Val	Arg	Tyr	His	Met	Ile	Lys	His	Pro	Ile	Ser	Asn
145					150					155					160

Asn	Leu	Thr	Ala	Asn	His	Gly	Tyr	Phe	Leu	Ile	Ala	Thr	Val	Trp	Thr
			165						170					175	

Leu	Gly	Phe	Ala	Ile	Cys	Ser	Pro	Leu	Pro	Val	Phe	His	Ser	Leu	Val
			180					185					190		

Glu	Leu	Lys	Glu	Thr	Phe	Gly	Ser	Ala	Leu	Leu	Ser	Ser	Lys	Tyr	Leu
		195					200					205			

Cys	Val	Glu	Ser	Trp	Pro	Ser	Asp	Ser	Tyr	Arg	Ile	Ala	Phe	Thr	Ile
	210					215					220				

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Ser	Leu	Leu	Leu	Val	Gln	Tyr	Ile	Leu	Pro	Leu	Val	Cys	Leu	Thr	Val
225					230					235					240
Ser	His	Thr	Ser	Val	Cys	Arg	Ser	Ile	Ser	Cys	Gly	Leu	Ser	His	Lys
				245					250					255	
Glu	Asn	Arg	Leu	Glu	Glu	Asn	Glu	Met	Ile	Asn	Leu	Thr	Leu	Gln	Pro
			260					265					270		
Ser	Lys	Lys	Ser	Arg	Asn	Gln	Ala	Lys	Thr	Pro	Ser	Thr	Gln	Lys	Trp
		275					280					285			
Ser	Tyr	Ser	Phe	Ile	Arg	Lys	His	Arg	Arg	Arg	Tyr	Ser	Lys	Lys	Thr
	290					295					300				
Ala	Cys	Val	Leu	Pro	Ala	Pro	Ala	Gly	Pro	Ser	Gln	Gly	Lys	His	Leu
305					310					315					320
Ala	Val	Pro	Glu	Asn	Pro	Ala	Ser	Val	Arg	Ser	Gln	Leu	Ser	Pro	Ser
				325					330					335	
Ser	Lys	Val	Ile	Pro	Gly	Val	Pro	Ile	Cys	Phe	Glu	Val	Lys	Pro	Glu
			340					345					350		
Glu	Ser	Ser	Asp	Ala	His	Glu	Met	Arg	Val	Lys	Arg	Ser	Ile	Thr	Arg
		355					360					365			
Ile	Lys	Lys	Arg	Ser	Arg	Ser	Val	Phe	Tyr	Arg	Leu	Thr	Ile	Leu	Ile
	370					375					380				
Leu	Val	Phe	Ala	Val	Ser	Trp	Met	Pro	Leu	His	Val	Phe	His	Val	Val
385					390					395					400
Thr	Asp	Phe	Asn	Asp	Asn	Leu	Ile	Ser	Asn	Arg	His	Phe	Lys	Leu	Val
			405						410					415	
Tyr	Cys	Ile	Cys	His	Leu	Leu	Gly	Met	Met	Ser	Cys	Cys	Leu	Asn	Pro
			420					425					430		
Ile	Leu	Tyr	Gly	Phe	Leu	Asn	Asn	Gly	Ile	Lys	Gln	Arg	Asp	Leu	Gln
		435					440					445			
Phe	Phe	Phe	Asn	Phe	Cys	Asp	Phe	Arg	Ser	Arg	Asp	Asp	Asp	Tyr	Glu
	450					455					460				
Thr	Ile	Ala	Met	Ser	Thr	Met	His	Thr	Asp	Val	Ser	Lys	Thr	Ser	Leu
465					470					475					480
Lys	Gln	Ala	Ser	Pro	Val	Ala	Phe	Lys	Lys	Ile	Ser	Met	Asn	Asp	Asn
				485					490					495	
Glu	Lys	Ile													

<210> 25  
<211> 395

105310 "GSSP" 766



Phe Tyr Arg Leu Thr Ile Leu Ile Leu Val Phe Ala Val Ser Trp Met  
 275 280 285  
 Pro Leu His Val Phe His Val Val Thr Asp Phe Asn Asp Asn Leu Ile  
 290 295 300  
 Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile Cys His Leu Leu Gly  
 305 310 315 320  
 Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr Gly Phe Leu Asn Asn  
 325 330 335  
 Gly Ile Lys Gln Arg Asp Leu Gln Phe Phe Phe Asn Phe Cys Asp Phe  
 340 345 350  
 Arg Ser Arg Asp Asp Asp Tyr Glu Thr Ile Ala Met Ser Thr Met His  
 355 360 365  
 Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser Pro Val Ala Phe  
 370 375 380  
 Lys Lys Ile Ser Met Asn Asp Asn Glu Lys Ile  
 385 390 395

<210> 26  
 <211> 341  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 26  
 Met Gly Ser Glu Ile Pro Asp Tyr Tyr Asn Lys Thr Leu Ala Ser Glu  
 1 5 10 15  
 Asn Asn Thr Val Ala Thr Arg Asn Ser Gly Phe Pro Val Trp Glu Asp  
 20 25 30  
 Tyr Lys Gly Ser Val Asp Asp Leu Gln Tyr Phe Leu Ile Gly Leu Tyr  
 35 40 45  
 Thr Phe Val Ser Leu Leu Gly Phe Met Gly Asn Leu Leu Ile Leu Met  
 50 55 60  
 Ala Val Met Arg Lys Arg Asn Gln Lys Thr Thr Val Asn Phe Leu Ile  
 65 70 75 80  
 Gly Asn Leu Ala Phe Ser Asp Ile Leu Val Val Leu Phe Cys Ser Pro  
 85 90 95  
 Phe Thr Leu Thr Ser Val Leu Leu Asp Gln Trp Met Phe Gly Lys Val  
 100 105 110  
 Met Cys His Ile Met Pro Phe Leu Gln Cys Val Thr Val Leu Val Ser



Thr Leu Ile Leu Ile Ser Ile Ala Ile Val Arg Tyr His Met Ile Lys  
130 135 140

His Pro Val Ser Asn Asn Leu Thr Ala Asn His Gly Tyr Phe Leu Ile  
145 150 155 160

Ala Thr Val Trp Thr Leu Gly Leu Ala Ile Cys Ser Pro Leu Pro Val  
165 170 175

Phe His Ser Leu Val Glu Leu Gln Glu Ser Phe Gly Ser Ala Trp Leu  
180 185 190

Ser Ser Arg Tyr Leu Cys Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg  
195 200 205

Ile Ala Phe Thr Ile Ser Leu Leu Leu Val Gln Tyr Ile Leu Pro Leu  
210 215 220

Val Cys Leu Thr Val Ser His Thr Ser Val Cys Ile Arg Leu Lys Arg  
225 230 235 240

Arg Asn Asn Met Met Asp Lys Met Arg Asp Asn Lys Tyr Arg Ser Ser  
245 250 255

Arg Ser Arg Ser Val Phe Tyr Arg Leu Thr Val Leu Ile Leu Val Phe  
260 265 270

Ala Val Ser Trp Met Pro Leu His Leu Phe His Val Val Thr Asp Phe  
275 280 285

Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val Tyr Cys Ile  
290 295 300

Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro Ile Leu Tyr  
305 310 315 320

Gly Phe Leu Asn Asn Gly Ile Lys Ala Asp Leu Met Ser Leu Ile His  
325 330 335

Cys Leu His Val Ser  
340

<210> 27  
<211> 383  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Y1/Y5 CHIMERA

<400> 27  
Met Gly Ser Glu Ile Pro Asp Tyr Tyr Asn Lys Thr Leu Ala Ser Glu  
1 5 10 15



Gly Phe Leu Asn Asn Gly Ile Gln Arg Asp Leu Gln Phe Phe Phe Asn  
325 330 335

Phe Cys Asp Phe Arg Ser Arg Asp Asp Asp Tyr Glu Val Ile Ala Met  
340 345 350

Ser Thr Met His Thr Asp Val Ser Lys Thr Ser Leu Lys Gln Ala Ser  
355 360 365

Pro Val Ala Leu Lys Lys Ile His Ser Asp Asp Asn Glu Lys Ile  
370 375 380

<210> 28

<211> 21

<212> DNA

<213> Homo sapiens

<400> 28

ttttggttgc tgacaaatgt c

21

<210> 29

<211> 26

<212> DNA

<213> Homo sapiens

<400> 29

ccttggtaaa cagtgagaat tattac

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Gly Phe Met Gly Asn Leu Leu Ile Leu Met Ala Leu Met Lys Lys Arg  
65 70 75 80

Asn Gln Lys Thr Thr Val Asn Phe Leu Ile Gly Asn Leu Ala Phe Ser  
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Asp Ile Leu Val Val Leu Phe Cys Ser Pro Phe Thr Leu Thr Ser Val  
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Leu Leu Asp Gln Trp Met Phe Gly Lys Val Met Cys His Ile Met Pro  
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 Phe Leu Gln Cys Val Ser Val Leu Val Ser Thr Leu Ile Leu Ile Ser  
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 Ile Ala Ile Val Arg Tyr His Met Ile Lys His Pro Ile Ser Asn Asn  
 145 150 155 160  
 Leu Thr Ala Asn His Gly Tyr Phe Leu Ile Ala Thr Val Trp Thr Leu  
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 Gly Phe Ala Ile Cys Ser Pro Leu Pro Val Phe His Ser Leu Val Glu  
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 Val Glu Ser Trp Pro Ser Asp Ser Tyr Arg Ile Ala Phe Thr Ile Ser  
 210 215 220  
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 His Thr Ser Val Cys Arg Ser Ile Ser Cys Gly Leu Ser Asn Lys Glu  
 245 250 255  
 Asn Arg Leu Glu Glu Asn Glu Met Ile Asn Leu Thr Leu His Pro Ser  
 260 265 270  
 Arg Lys Ile Gly Pro Gln Val Lys Leu Ser Gly Ser His Lys Trp Ser  
 275 280 285  
 Tyr Ser Phe Ile Lys Lys His Arg Arg Arg Tyr Ser Lys Lys Thr Ala  
 290 295 300  
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 Ile Leu Pro Glu Asn Phe Gly Ser Val Arg Ser Gln Leu Ser Ser Ser  
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 Ser Lys Phe Ile Pro Gly Val Pro Thr Cys Phe Glu Ile Lys Pro Glu  
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 Glu Asn Ser Asp Val His Glu Leu Arg Val Lys Arg Ser Val Thr Arg  
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 Thr Asp Phe Asn Asp Asn Leu Ile Ser Asn Arg His Phe Lys Leu Val  
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Tyr Cys Ile Cys His Leu Leu Gly Met Met Ser Cys Cys Leu Asn Pro  
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